

NEW	10	20	30	40	50	60
HNCDNA . SEQ	ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC					
HN . SEQ	ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCGGCC					
OLD	10	20	30	40	50	60
HNCDNA . SEQ	CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT					
HN . SEQ	CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT					
	70	80	90	100	110	120
HNCDNA . SEQ	CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGAGGAGGCTCTTCTGGGGAA					
HN . SEQ	CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGAGGAGGCTCTTCTGGGGAA					
	130	140	150	160	170	180
HNCDNA . SEQ	GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT					
HN . SEQ	GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT					
	180	190	200	210	220	230
HNCDNA . SEQ	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT					
HN . SEQ	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT					
	240	250	260	270	280	290
HNCDNA . SEQ	GAAGTTAAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGT					
HN . SEQ	GAAGTTAATGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGT					
	300	310	320	330	340	350
HNCDNA . SEQ	TGAGGCTCCTGGAGATCCTCAAGAACCCAGATAATGCCACAGGGACAAAGAAGGGGA					
HN . SEQ	TGAGGCTCCTGGAGATCCTCAAGAACCCAGATAATGCCACAGGGACAAAGAAGGGGA					
	360	370	380	390	400	410
HNCDNA . SEQ	TGACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCTGGCCCCGGGTGTCCCCAGCCTG					
HN . SEQ	TGACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCTGGCCCCGGGTGTCCCCAGCCTG					
	420	430	440	450	460	470
HNCDNA . SEQ	CGCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCAGCTCGCCGCCTTCTGCCCCGGC					
HN . SEQ	CGCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCAGCTCGCCGCCTTCTGCCCCGGC					
	480	490	500	510	520	530
HNCDNA . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					
HN . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					
	540	550	560	570	580	590
HNCDNA . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					
HN . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					

	600	610	620	630	640	650
HNCDNA . SEQ	GAACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCC					
HN . SEQ	AGACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCC					
	600	610	620	630	640	650
HNCDNA . SEQ	CGGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGG					
HN . SEQ	CGGGCGGGAGTACC- GGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGG					
	660	670	680	690	700	710
HNCDNA . SEQ	CTCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAG					
HN . SEQ	CTCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAG					
	720	730	740	750	760	770
HNCDNA . SEQ	CACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCGGGAGGCCTGGCCGTGTTGGC					
HN . SEQ	CACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCGGGAGGCCTGGCCGTGTTGG-					
	780	790	800	810	820	830
HNCDNA . SEQ	CGCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTG-CCTATGAGCAGTTGCTGTCTCGCT					
HN . SEQ	CGCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGTCCTATGAGCAGTTGCTGTCTCGCT					
	840	850	860	870	880	890
HNCDNA . SEQ	TGGAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCAC					
HN . SEQ	TGGAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCAC					
	900	910	920	930	940	950
HNCDNA . SEQ	TCCTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCT					
HN . SEQ	TCCTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCT					
	960	970	980	990	1000	1010
HNCDNA . SEQ	GTGCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGC					
HN . SEQ	GTGCCCAGGGTGTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGC					
	1020	1030	1040	1050	1060	1070
HNCDNA . SEQ	TCCACACCCTCTCTGACACCCTGTGGGGACCTGGTGA CTCTCGGCTACAGCTGAACTTCC					
HN . SEQ	TCCACACCCTCTCTGACACCCTGTGGGGACCTGGTGA CTCTCGGCTACAGCTGAACTTCC					
	1080	1090	1100	1110	1120	1130
HNCDNA . SEQ	GAGCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACA					
HN . SEQ	GAGCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACA					
	1140	1150	1160	1170	1180	1190

	1200	1210	1220	1230	1240	1250
MNCDNA .SEQ	GCAGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCC					
	::					
MN .SEQ	GCAGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCC					
	1200	1210	1220	1230	1240	1250
MNCDNA .SEQ	1260	1270	1280	1290	1300	1310
	TAGCCCTGGTTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGA					
	::					
MN .SEQ	TAGCCCTGGTTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGA					
	1260	1270	1280	1290	1300	1310
MNCDNA .SEQ	1320	1330	1340	1350	1360	1370
	GAAGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGC-TACCGCCCAGCAGAGGTAGCC					
	::					
MN .SEQ	GAAGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCGTACCGCCCAGCAGAGGTAGCC					
	1320	1330	1340	1350	1360	1370
MNCDNA .SEQ	1380	1390	1400	1410	1420	1430
	GAGACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGA					
	::					
MN .SEQ	GAGACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGA					
	1380	1390	1400	1410	1420	1430
MNCDNA .SEQ	1440	1450	1460	1470	1480	1490
	GGGGGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAA					
	::					
MN .SEQ	GGGGGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAA					
	1440	1450	1460	1470	1480	1490
MNCDNA .SEQ	1500	1510	1520			
	ATTTTTTAAAATAAATATTTATAAT					
	:::::v^::::::::::::::::::::::::::::					
MN .SEQ	ATTTTTTAAAATAAATATTTATAAT					
	1500	1510	1520			